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APPLICATION NO.	FILING DATE	FIRST NAMED INVENTOR	ATTORNEY DOCKET NO.	CONFIRMATION NO.
10/015,392	12/12/2001	Kevin P. Baker	P2830P1C58	9874

7590 03/15/2004

Ginger R Dreger
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EXAMINER

LANDSMAN, ROBERT S

ART UNIT	PAPER NUMBER
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1647

DATE MAILED: 03/15/2004

Please find below and/or attached an Office communication concerning this application or proceeding.

Office Action Summary

Application No.

10/015,392

Applicant(s)

GENENTECH, INC.

Examiner

Robert Landsman

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-- The MAILING DATE of this communication appears on the cover sheet with the correspondence address --
Period for Reply

A SHORTENED STATUTORY PERIOD FOR REPLY IS SET TO EXPIRE 3 MONTH(S) FROM THE MAILING DATE OF THIS COMMUNICATION.

- Extensions of time may be available under the provisions of 37 CFR 1.136(a). In no event, however, may a reply be timely filed after SIX (6) MONTHS from the mailing date of this communication.
- If the period for reply specified above is less than thirty (30) days, a reply within the statutory minimum of thirty (30) days will be considered timely.
- If NO period for reply is specified above, the maximum statutory period will apply and will expire SIX (6) MONTHS from the mailing date of this communication.
- Failure to reply within the set or extended period for reply will, by statute, cause the application to become ABANDONED (35 U.S.C. § 133). Any reply received by the Office later than three months after the mailing date of this communication, even if timely filed, may reduce any earned patent term adjustment. See 37 CFR 1.704(b).

Status

- 1) ☐ Responsive to communication(s) filed on ____.
- 2a) ☐ This action is **FINAL**. 2b) ☒ This action is non-final.
- 3) ☐ Since this application is in condition for allowance except for formal matters, prosecution as to the merits is closed in accordance with the practice under *Ex parte Quayle*, 1935 C.D. 11, 453 O.G. 213.

Disposition of Claims

- 4) ☒ Claim(s) 28-47 is/are pending in the application.
- 4a) Of the above claim(s) ____ is/are withdrawn from consideration.
- 5) ☐ Claim(s) ____ is/are allowed.
- 6) ☒ Claim(s) 28-47 is/are rejected.
- 7) ☐ Claim(s) ____ is/are objected to.
- 8) ☐ Claim(s) ____ are subject to restriction and/or election requirement.

Application Papers

- 9) ☒ The specification is objected to by the Examiner.
- 10) ☒ The drawing(s) filed on 12 December 2001 is/are: a) ☒ accepted or b) ☐ objected to by the Examiner.
Applicant may not request that any objection to the drawing(s) be held in abeyance. See 37 CFR 1.85(a).
Replacement drawing sheet(s) including the correction is required if the drawing(s) is objected to. See 37 CFR 1.121(d).
- 11) ☐ The oath or declaration is objected to by the Examiner. Note the attached Office Action or form PTO-152.

Priority under 35 U.S.C. § 119

- 12) ☐ Acknowledgment is made of a claim for foreign priority under 35 U.S.C. § 119(a)-(d) or (f).
- a) ☐ All b) ☐ Some * c) ☐ None of:
- ☐ Certified copies of the priority documents have been received.
 - ☐ Certified copies of the priority documents have been received in Application No. ____.
 - ☐ Copies of the certified copies of the priority documents have been received in this National Stage application from the International Bureau (PCT Rule 17.2(a)).

* See the attached detailed Office action for a list of the certified copies not received.

Attachment(s)

- 1) ☒ Notice of References Cited (PTO-892)
- 2) ☐ Notice of Draftsperson's Patent Drawing Review (PTO-948)
- 3) ☒ Information Disclosure Statement(s) (PTO-1449 or PTO/SB/08)
Paper No(s)/Mail Date 9/17/02, 11/14/02
- 4) ☐ Interview Summary (PTO-413)
Paper No(s)/Mail Date. ____.
- 5) ☐ Notice of Informal Patent Application (PTO-152)
- 6) ☒ Other: Sequence Comparisons A-C.

DETAILED ACTION

1. Formal Matters

12/12/01

m
3/11/04

- A. The Preliminary Amendment dated ~~12/7/01~~, has been entered into the record.
- B. Claims 28-47 are pending and are the subject of this Office Action.

2. Priority

Due to the excessive number of applications from which the present application claims benefit, priority cannot be determined. However, the Examiner has concluded that the subject matter defined in this application is not supported by any of the applications in the chain of priority because the presently claimed subject matter is not supported by a specific, substantial or well-established utility, nor, for this reason, is it enabled. Accordingly, the subject matter defined in claims 28-47 has an effective filing date of 12/12/01, which is the filing date of the present application.

Should the applicant disagree with the examiner's factual determination above, it is incumbent upon the applicant to provide the serial number and specific page number(s) of any parent application filed prior to 12/12/01 which specifically supports the particular claim limitation for each and every claim limitation in all the pending claims which applicant considers to have been in possession of and fully enabled for prior to 12/12/01.

3. Information Disclosure Statement

- A. Reference 1 on the IDS dated 9/17/02 and reference 1 on the IDS dated 11/14/02 have been lined through since they are not in proper format, including author and accession number.

4. Specification

- A. Though none could be found, due to the length of the specification, Applicants are reminded that embedded hyperlink and/or other form of browser-executable code are not permitted in the specification. See MPEP § 608.01.
- B. The title of the invention is not descriptive. A new title is required that is clearly indicative of the invention to which the claims are directed. The title recites polypeptides and polynucleotides whereas the claims are drawn to polynucleotides.

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5. Claim Objections

A. The syntax of claims 28-47 could be improved by replacing the phrase "shown in Figure 152 (SEQ ID NO:271)" with "of SEQ ID NO:271" and "shown in Figure 151 (SEQ ID NO:270)" with "of SEQ ID NO:270" where appropriate.

6. Claim Rejections - 35 USC § 101

35 U.S.C. 101 reads as follows:

Whoever invents or discovers any new and useful process, machine, manufacture, or composition of matter, or any new and useful improvement thereof, may obtain a patent therefor, subject to the conditions and requirements of this title.

A. Claims 28-47 are rejected under 35 U.S.C. 101 because the claimed invention is not supported by a specific, substantial and credible asserted utility or a well established utility. These claims are directed to polynucleotides homologous to SEQ ID NO:270 encoding polypeptides having various sequence homology to SEQ ID NO:271. However, the invention encompassed by these claims has no apparent or disclosed patentable utility. This rejection is consistent with the current utility guidelines, published 1/5/01, 66 FR 1092. The instant application has provided a description of an isolated protein. However, the instant application does not disclose a specific and substantial biological role of this protein or its significance.

However, it is clear from the instant specification that the claimed protein is what is termed an "orphan receptor" in the art. The instant application does not disclose the biological role of the claimed protein or its significance. Applicants disclose in the specification that the receptor has certain amino acid sequence identity with the following Dayhoff sequences: I48652, P_R76466, HSMHC3W36A_2, EPB4 HUMAN, P_R14256, EPA8 MOUSE, P_R77285, P_W13569, AF000560_1, and ASF1_HELAN. However, homology alone is not sufficient to demonstrate utility of the present invention. There is little doubt that, after complete characterization, this protein will probably be found to have a patentable utility. This further characterization, however, is part of the act of invention and, until it has been undertaken, Applicants' claimed invention is incomplete.

The instant situation is directly analogous to that of which was addressed in *Brenner v. Manson*, 148 U.S.P.Q. 689 (Sus. Ct, 1966), in which a novel compound which was structurally analogous to other compounds which were known to possess anticancer activity was alleged to be potentially useful as an antitumor agent in the absence of evidence supporting this utility. The court expressed the opinion that all chemical compounds are "useful" to the chemical arts when this term is given its broadest interpretation. However, the court held that this broad interpretation was not the intended definition of "useful" as it

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appears in 35 U.S.C. 101, which required that an invention must have either an immediate obvious or fully disclosed "real-world" utility. The court held that:

"The basic quid pro quo contemplated by the Constitution and the Congress for granting a patent monopoly is the benefit derived by the public from an invention with substantial utility," "[u]nless and until a process is refined and developed to this point - where specific benefit exists in currently available form - there is insufficient justification for permitting an applicant to engross what may prove to be a broad field," and "a patent is not a hunting license," "[i]t is not a reward for the search, but compensation for its successful conclusion."

The specification discloses that the polynucleotides of the invention encode proteins which have significant sequence similarity to known proteins. Based on the structural similarity, the specification asserts that the newly disclosed SEQ ID NO:271, and its encoding polynucleotides have similar activities. The assertion that the disclosed proteins have biological activities similar to known proteins cannot be accepted in the absence of supporting evidence, because generally, the art acknowledges that function cannot be predicted based solely on structural similarity to a protein found in the sequence databases. For example, Skolnick et al. (2000, Trends in Biotech. 18:34-39) state that knowing the protein structure by itself is insufficient to annotate a number of functional classes, and is also insufficient for annotating the specific details of protein function (see Box 2, p. 36). Similarly, Bork (2000, Genome Research 10:398-400) states that the error rate of functional annotations in the sequence database is considerable, making it even more difficult to infer correct function from a structural comparison of a new sequence with a sequence database (see especially p. 399). Such concerns are also echoed by Doerks et al. (1998, Trends in Genetics 14:248-250) who state that (1) functional information is only partially annotated in the database, ignoring multi functionality, resulting in underpredictions of functionality of a new protein and (2) overpredictions of functionality occur because structural similarity often does not necessarily coincide with functional similarity. Smith et al. (1997, Nature Biotechnology 15:1222-1223) remark that there are numerous cases in which proteins having very different functions share structural similarity due to evolution from a common ancestral gene.

Brenner (1999, Trends in Genetics 15:132-133) argues that accurate inference of function from homology must be a difficult problem since, assuming there are only about 1000 major gene superfamilies in nature, then most homologs must have different molecular and cellular functions. Finally, Bork et al. (1996, Trends in Genetics 12:425-427) add that the software robots that assign functions to new proteins often assign a function to a whole new protein based on structural similarity of a small domain of the new protein to a small domain of a known protein. Such questionable interpretations are written into the sequence database and are then considered facts.

Therefore, based on the discussions above concerning the specific examples of structurally similar proteins that have different functions, along with the art's recognition that one cannot rely upon structural similarity alone to determine functionality, the specification fails to teach the skilled artisan the utility of the protein of SEQ ID NO:271 which is only known to be homologous to various receptors. Therefore, the instant claims are drawn to a protein, or a polynucleotide encoding a protein which has a yet undetermined function or biological significance. There is no actual and specific significance which can be attributed to said protein identified in the specification. For this reason, the instant invention is incomplete. In the absence of a knowledge of the natural ligands or biological significance of this protein, there is no immediately obvious patentable use for it. To employ a protein of the instant invention in the identification of substances which bind to and/or mediate activity of the said receptor is clearly to use it as the object of further research which has been determined by the courts to be a non-patentable utility. Since the instant specification does not disclose a "real-world" use for said protein then the claimed invention is incomplete and, therefore, does not meet the requirements of 35 U.S.C. 101 as being useful.

Applicants demonstrate that the present invention is positive in the mixed lymphocyte reaction assay. However, the fact that this protein is inhibitory in this assay does not demonstrate a specific and substantial utility, or a well-established utility.

Furthermore, since the protein of the invention is not supported by a specific and substantial asserted utility or a well established utility, the encoding polynucleotides, vectors, host cells and methods of making proteins also lack utility.

7. Claim Rejections - 35 USC § 112, first paragraph - enablement

The following is a quotation of the first paragraph of 35 U.S.C. 112:

The specification shall contain a written description of the invention, and of the manner and process of making and using it, in such full, clear, concise, and exact terms as to enable any person skilled in the art to which it pertains, or with which it is most nearly connected, to make and use the same and shall set forth the best mode contemplated by the inventor of carrying out his invention.

A. Claims 28-47 are rejected under 35 U.S.C. 112, first paragraph, as failing to adequately teach how to use the instant invention. Specifically, since the claimed invention is not supported by a specific, substantial and credible asserted utility or a well established utility for the reasons set forth above, one skilled in the art clearly would not know how to use the claimed invention.

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B. Claims 28-47 are rejected under 35 U.S.C. 112, first paragraph, as containing subject matter which was not described in the specification in such a way as to enable one skilled in the art to which it pertains, or with which it is most nearly connected, to make and/or use the invention.

The deposit of the biological material is considered necessary for the enablement of the current invention (see MPEP Chapter 2400 and 37 C.F.R. §§ 1.801-1.809). Elements required for practicing a claimed invention must be known and readily available to the public or obtainable by a repeatable method set forth in the specification. If a deposit (203277) is made under the terms of the Budapest Treaty on the International Recognition of the Deposit of Microorganisms for the Purposes of Patent Procedure (e.g. see 961 OG 21, 1977), and Applicants, their assignee or their agent needs to provide a declaration containing the following:

1. the current address of the ATCC.
2. a declaration, or statement over attorney's signature stating that all restrictions imposed by the depositor on the availability to the public of the deposited biological material be irrevocably removed upon the granting of the patent (see MPEP Chapter 2410.01 and 37 C.F.R. § 1.808).

C. Furthermore, even if the claims possessed utility under 35 USC 101, claims 28-47 would still be rejected under 35 USC 112, first paragraph, because the specification, while then being enabling for SEQ ID NO:270 and 271, does not reasonably provide enablement for polynucleotides or polypeptides having at least 80%, 85%, 90%, 95% or 99% sequence identity to SEQ ID NO:270 or 271, to the protein encoded by ATCC No. 203277, for the extracellular domain thereof, or for vectors and host cells containing these polynucleotides. The specification does not enable any person skilled in the art to which it pertains, or with which it is most nearly connected, to make the invention commensurate in scope with these claims. There is no functional limitation in the claims. The claims encompass an unreasonable number of inoperative polypeptides, or polynucleotides which encode these polypeptides, which the skilled artisan would not know how to use.

There are no working examples of polynucleotides or polypeptides less than 100% identical to SEQ ID NO:270 or 271, or the mature form thereof (i.e. lacking its signal peptide). The skilled artisan would not know how to use non-identical polypeptides or polynucleotides on the basis of teachings in the prior art or specification unless they possessed a specific function disclosed in the instant specification, in which there is none. While the specification generally describes homologous proteins, Applicants still have not taught to which family of proteins the protein of the present invention belongs. The specification does not provide guidance for using polynucleotides encoding polypeptides related to (*i.e.*, 80%-99% identity) but not identical to SEQ ID NO:270 or 271 which do not have any specific, known function.

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The claims are broad because they do not require the claimed polypeptide to be identical to the disclosed sequence and because the claims have no functional limitation.

For these reasons, which include the complexity and unpredictability of the nature of the invention and art in terms of the diversity of proteins and lack of knowledge about function(s) of encompassed polypeptides structurally related to SEQ ID NO:271, or their encoding polynucleotides (e.g. SEQ ID NO:270) the lack of direction or guidance for using polypeptides that are not identical to SEQ ID NO:271, and the breadth of the claims for structure without function, it would require undue experimentation to use the invention commensurate in scope with the claims.

8. Claim Rejections - 35 USC § 112, first paragraph – written description

A. Claims 28-47 are rejected under 35 U.S.C. 112, first paragraph, as containing subject matter which was not described in the specification in such a way as to reasonably convey to one skilled in the relevant art that the inventor(s), at the time the application was filed, had possession of the claimed invention.

The claims are drawn to polynucleotides having at least 80%, 85%, 90%, 95% or 99% sequence identity with SEQ ID NO:270 as well as vectors and host cells. The claims do not require that the polynucleotides or encoded polypeptides of the present invention possess any particular biological activity, nor any particular conserved structure, or other disclosed distinguishing feature. Thus, the claims are drawn to a genus of polypeptides that is defined only by sequence identity.

To provide adequate written description and evidence of possession of a claimed genus, the specification must provide sufficient distinguishing identifying characteristics of the genus. The factors to be considered include disclosure of complete or partial structure, physical and/or chemical properties, functional characteristics, structure/function correlation, methods of making the claimed product, or any combination thereof. In this case, the only factor present in the claim is a partial structure in the form of a recitation of percent identity. There is not even identification of any particular portion of the structure that must be conserved. Accordingly, in the absence of sufficient recitation of distinguishing identifying characteristics, the specification does not provide adequate written description of the claimed genus.

Vas-Cath Inc. v. Mahurkar, 19USPQ2d 1111, clearly states “applicant must convey with reasonable clarity to those skilled in the art that, as of the filing date sought, he or she was in possession of the invention. The invention is, for purposes of the ‘written description’ inquiry, *whatever is now claimed*.” (See page 1117.) The specification does not “clearly allow persons of ordinary skill in the art to recognize that [he or she] invented what is claimed.” (See *Vas-Cath* at page 1116). As discussed above,

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the skilled artisan cannot envision the detailed chemical structure of the encompassed genus of polypeptides, and therefore conception is not achieved until reduction to practice has occurred, regardless of the complexity or simplicity of the method of isolation. Adequate written description requires more than a mere statement that it is part of the invention and reference to a potential method of isolating it. The compound itself is required. See *Fiers v. Revel*, 25 USPQ2d 1601 at 1606 (CAFC 1993) and *Amgen Inc. v. Chugai Pharmaceutical Co. Ltd.*, 18 USPQ2d 1016.

One cannot describe what one has not conceived. See *Fiddes v. Baird*, 30 USPQ2d 1481 at 1483. In *Fiddes*, claims directed to mammalian FGF's were found to be unpatentable due to lack of written description for that broad class. The specification provided only the bovine sequence.

Therefore, only isolated polypeptides comprising the amino acid sequence set forth in SEQ ID NO:271, or encoded by SEQ ID NO:270, but not the full breadth of the claims, meets the written description provision of 35 U.S.C. §112, first paragraph. Applicant is reminded that *Vas-Cath* makes clear that the written description provision of 35 U.S.C. §112 is severable from its enablement provision (see page 1115).

9. Claim Rejections - 35 USC § 112, second paragraph

The following is a quotation of the second paragraph of 35 U.S.C. 112:

The specification shall conclude with one or more claims particularly pointing out and distinctly claiming the subject matter which the applicant regards as his invention.

Claims 28-47 are rejected under 35 U.S.C. 112, second paragraph, as being indefinite for failing to particularly point out and distinctly claim the subject matter which applicant regards as the invention.

A. Claims 28-47 are vague and indefinite since it is not clear whether or not the protein encoded by the polynucleotide of the present invention is a soluble protein (e.g protease), nor is it disclosed as being expressed on a cell surface. Accordingly, the limitation that the claimed protein comprises an "extracellular domain" is indefinite, as the art does not recognize soluble proteins as having such domains. Further, if the protein had an extracellular domain, the recitation of "the extracellular domain"... "lacking its associated signal sequence" is indefinite as a signal sequence is not generally considered to be part of an extracellular domain, as signal sequences are cleaved from said domains in the process of secretion from the cell.

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B. Claims 41-43 are vague and indefinite since the claim recites "hybridizes" without the recitation of any conditions, or recites "stringent conditions: wherein these conditions are not known. Nucleic acid molecules which hybridize under conditions of "low" stringency would not necessarily hybridize under conditions of "high" stringency. Furthermore, not all conditions of "high" or "low" stringency, for example, are the same. Therefore, it is required that Applicants amend the claims to recite the exact hybridization conditions without using indefinite phrases such as "*for example*" **without adding new matter**.

10. Claim Rejections - 35 USC § 102

The following is a quotation of the appropriate paragraphs of 35 U.S.C. 102 that form the basis for the rejections under this section made in this Office action:

A person shall be entitled to a patent unless –

(b) the invention was patented or described in a printed publication in this or a foreign country or in public use or on sale in this country, more than one year prior to the date of application for patent in the United States.

A. Claims 28-47 are rejected under 35 U.S.C. 102(b) as being anticipated by Ashkenazi et al. (WO 00/53758). The claims recite a polynucleotide at least 80% identical to that of SEQ ID NO:270 or encoding SEQ ID NO:271, as well as fragments (e.g. extracellular domains, with and without signal sequence – see, e.g., page 3, line 25 – page 4, line 10) thereof. The claims also recite nucleic acid molecules which hybridize to SEQ ID NO:270, or one encoding SEQ ID NO:271 as well as vectors and host cells. Ashkenazi teach a polynucleotide which is 100% identical to SEQ ID NO:270 (Sequence Comparisons C) and which encodes the polypeptide of SEQ ID NO:271 (Sequence Comparisons A and B) as well as vectors and host cells (pages 2-6. This nucleic acid molecule will hybridize to that of the present invention even under the most stringent conditions.

11. Conclusion

A. No claim is allowable.

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Advisory information

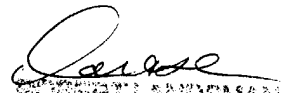
Any inquiry concerning this communication or earlier communications from the examiner should be directed to Robert Landsman whose telephone number is (703) 306-3407. The examiner can normally be reached on Monday - Friday from 8:00 AM to 5:00 PM (Eastern time) and alternate Fridays from 8:00 AM to 5:00 PM (Eastern time).

If attempts to reach the examiner by telephone are unsuccessful, the Examiner's supervisor, Gary Kunz, can be reached on (703) 308-4623.

Official papers filed by fax should be directed to (703) 308-4242. Fax draft or informal communications with the examiner should be directed to (703) 308-0294.

Any inquiry of a general nature or relating to the status of this application or proceeding should be directed to the Group receptionist whose telephone number is (703) 308-0196.

Robert Landsman, Ph.D.
Patent Examiner
Group 1600
March 12, 2004


ROBERT LANDSMAN
PATENT EXAMINER

Sequence Comparison A

ID AAB33455 standard; Protein; 238 AA.
XX
DT 29-JAN-2001 (first entry)
XX
DE Human PR01410 protein UNQ728 SEQ ID NO:189.
XX
OS Homo sapiens.
XX
PN WO200053758-A2.
XX
PD 14-SEP-2000.
XX
PF 02-MAR-2000; 2000WO-US05841.
XX
PR 08-MAR-1999; 99WO-US05028.
PR 10-MAR-1999; 99US-0123618.
PR 12-MAR-1999; 99US-0123957.
PR 23-MAR-1999; 99US-0125775.
PR 12-APR-1999; 99US-0128849.
PR 20-APR-1999; 99WO-US08615.
PR 28-APR-1999; 99US-0131445.
PR 04-MAY-1999; 99US-0132371.
PR 14-MAY-1999; 99US-0134287.
PR 02-JUN-1999; 99WO-US12252.
PR 23-JUN-1999; 99US-0141037.
PR 20-JUL-1999; 99US-0144758.
PR 26-JUL-1999; 99US-0145698.
PR 28-JUL-1999; 99US-0146222.
PR 01-SEP-1999; 99WO-US20111.
PR 08-SEP-1999; 99WO-US20594.
PR 13-SEP-1999; 99WO-US20944.
PR 15-SEP-1999; 99WO-US21090.
PR 15-SEP-1999; 99WO-US21547.
PR 05-OCT-1999; 99WO-US23089.
PR 29-OCT-1999; 99US-0162506.
PR 29-NOV-1999; 99WO-US28214.
PR 30-NOV-1999; 99WO-US28313.
PR 30-NOV-1999; 99WO-US28409.
PR 01-DEC-1999; 99WO-US28301.
PR 01-DEC-1999; 99WO-US28634.
PR 02-DEC-1999; 99WO-US28551.
PR 02-DEC-1999; 99WO-US28564.
PR 02-DEC-1999; 99WO-US28565.
PR 16-DEC-1999; 99WO-US30095.
PR 20-DEC-1999; 99WO-US30999.
PR 30-DEC-1999; 99WO-US31274.
PR 05-JAN-2000; 2000WO-US00219.
PR 06-JAN-2000; 2000WO-US00277.
PR 06-JAN-2000; 2000WO-US00376.
PR 11-FEB-2000; 2000WO-US03565.
PR 18-FEB-2000; 2000WO-US04341.
PR 18-FEB-2000; 2000WO-US04342.
PR 22-FEB-2000; 2000WO-US04414.
XX
PA (GETH) GENENTECH INC.
XX
PI Ashkenazi AJ, Baker KP, Goddard A, Gurney AL, Hebert C, Henzel W;
PI Kabakoff RC, Lu Y, Pan J, Pennica D, Shelton DL, Smith V;
PI Stewart TA, Tumas D, Watanabe CK, Wood WI, Yan M;
XX
DR WPI; 2000-572271/53.
DR N-PSDB; AAC58620.
XX

XX
PS Claim 33; Fig 84; 309pp; English.

SQ Sequence 238 AA;

Query Match 100.0%; Score 1300; DB 21; Length 238;
Best Local Similarity 100.0%; Pred. No. 1.6e-114;
Matches 238; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy	1	MLGSPCLLWLLAVTFLVPRAQPLAQDFEEEEADETETAWPPLPAVPCDYDHCRLQVPC	60
Db	1	MLGSPCLLWLLAVTFLVPRAQPLAQDFEEEEADETETAWPPLPAVPCDYDHCRLQVPC	60
Qy	61	KELQRVGPAACLCPGLSSPAQPPDPFRMGVEVRIAAEEGRAVVHWCAPFSPVLHYWLLLD	120
Db	61	KELQRVGPAACLCPGLSSPAQPPDPFRMGVEVRIAAEEGRAVVHWCAPFSPVLHYWLLLD	120
Qy	121	GSEAAQKGPPPLNATVRRaelKGLKPGGIYVVCVVAANEAGASRPQAGGEGLEGADIPAF	180
Db	121	GSEAAQKGPPPLNATVRRaelKGLKPGGIYVVCVVAANEAGASRPQAGGEGLEGADIPAF	180
Qy	181	GPCSRLAVPPNPRTLVAHAVGVGTALALLSCAALVWHFCLDRWGCPRAAARAAGAL	238
Db	181	GPCSRLAVPPNPRTLVAHAVGVGTALALLSCAALVWHFCLDRWGCPRAAARAAGAL	238

ID AAC58620 standard; cDNA; 1170 BP. *Sequence*
 XX
 AC AAC58620;
 XX
 DT 29-JAN-2001 (first entry)
 XX
 DE Human PRO1410 protein UNQ728 encoding cDNA SEQ ID NO:188.
 XX
 PN WO200053758-A2.
 XX
 PD 14-SEP-2000.

SQ Sequence 1170 BP; 213 A; 376 C; 377 G; 204 T; 0 other;

Alignment Scores:

Pred. No.:	1.8e-76	Length:	1170
Score:	1300.00	Matches:	238
Percent Similarity:	100.00%	Conservative:	0
Best Local Similarity:	100.00%	Mismatches:	0
Query Match:	100.00%	Indels:	0
DB:	21	Gaps:	0

US-10-011-795B-271 (1-238) x AAC58620 (1-1170)

Sequence Comparison B

Qy 1 MetLeuGlySerProCysLeuLeuTrpLeuLeuAlaValThrPheLeuValProArgAla 20
 Db 152 ATGCTGGGCTCTCCCTGCCTTCTGTGGCTCCTGGCCGTGACCTTCTTGGTTCCAGAGCT 211
 Qy 21 GlnProLeuAlaProGlnAspPheGluGluGluGluAlaAspGluThrGluThrAlaTrp 40
 Db 212 CAGCCCTTGGCCCCCTCAAGACTTTGAAGAAGAGGAGGCAGATGAGACTGAGACGGCGTGG 271
 Qy 41 ProProLeuProAlaValProCysAspTyrAspHisCysArgHisLeuGlnValProCys 60
 Db 272 CCGCCTTTGCCGGCTGTCCCCTGCGACTACGACCACTGCCGACACCTGCAGGTGCCCTGC 331
 Qy 61 LysGluLeuGlnArgValGlyProAlaAlaCysLeuCysProGlyLeuSerSerProAla 80
 Db 332 AAGGAGCTACAGAGGGTCGGGCCGGCGGCCTGCCTGTGCCAGGACTCTCCAGCCCCGCC 391
 Qy 81 GlnProProAspProProArgMetGlyGluValArgIleAlaAlaGluGluGlyArgAla 100
 Db 392 CAGCCGCCCCGACCCGCGCATGGGAGAAGTGCGCATTGCGGCCGAAGAGGGCCGCGCA 451
 Qy 101 ValValHisTrpCysAlaProPheSerProValLeuHisTyrTrpLeuLeuLeuTrpAsp 120
 Db 452 GTGGTCCACTGGTGTGCCCCCTTCTCCCCGGTCTCCACTACTGGCTGCTGCTTTGGGAC 511
 Qy 121 GlySerGluAlaAlaGlnLysGlyProProLeuAsnAlaThrValArgArgAlaGluLeu 140
 Db 512 GGCAGCGAGGCTGCGCAGAAGGGGCCCGCTGAACGCTACGGTCCGAGAGCCGAAGT 571
 Qy 141 LysGlyLeuLysProGlyGlyIleTyrValValCysValValAlaAlaAsnGluAlaGly 160
 Db 572 AAGGGGCTGAAGCCAGGGGGCATTATATGTCGTTTGCGTAGTGGCCGCTAACGAGGCCGGG 631
 Qy 161 AlaSerArgValProGlnAlaGlyGlyGluGlyLeuGluGlyAlaAspIleProAlaPhe 180
 Db 632 GCAAGCCGCTGCCCCAGGCTGGAGGAGAGGGCCTCGAGGGGGCCGACATCCCTGCCTTC 691
 Qy 181 GlyProCysSerArgLeuAlaValProProAsnProArgThrLeuValHisAlaAlaVal 200
 Db 692 GGGCCTTGACGCGCCTTGCGGTGCCGCCCAACCCCGCACTCTGGTCCACGCGGCCGTC 751
 Qy 201 GlyValGlyThrAlaLeuAlaLeuLeuSerCysAlaAlaLeuValTrpHisPheCysLeu 220
 Db 752 GGGGTGGGCACGGCCCTGGCCCTGCTAAGCTGTGCCGCCCTGGTGTGGCACTTCTGCCTG 811
 Qy 221 ArgAspArgTrpGlyCysProArgArgAlaAlaAlaArgAlaAlaGlyAlaLeu 238
 Db 812 CGCGATCGCTGGGGCTGCCCGCGCCGAGCCGCCCGAGCCGAGGGGCGCTC 865

ID AAC58620 standard; cDNA; 1170 BP.
 XX
 AC AAC58620;
 XX
 DT 29-JAN-2001 (first entry)
 XX
 DE Human PRO1410 protein UNQ728 encoding cDNA SEQ ID NO:188.
 XX
 PN WO200053758-A2.
 XX
 PD 14-SEP-2000.
 XX
 PF 02-MAR-2000; 2000WO-US05841.
 XX
 SQ Sequence 1170 BP; 213 A; 376 C; 377 G; 204 T; 0 other;

Query Match 100.0%; Score 1170; DB 21; Length 1170;
Best Local Similarity 100.0%; Pred. No. 6.6e-239;
Matches 1170; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy	1	GTCTGAAGGTTTATAAAAGCTTCCAGCCAAACGGCATTGAAGTTGAAGATACAACCTGACAG	60
Db	1	GTCTGAAGGTTTATAAAAGCTTCCAGCCAAACGGCATTGAAGTTGAAGATACAACCTGACAG	60
Qy	61	CACAGCCTGAGATCTTGGGGATCCCTCAGCCTAACACCCACAGACGTCAGCTGGTGGATT	120
Db	61	CACAGCCTGAGATCTTGGGGATCCCTCAGCCTAACACCCACAGACGTCAGCTGGTGGATT	120
Qy	121	CCCGCTGCATCAAGGCCTACCCACTGTCTCCATGCTGGGCTCTCCCTGCCTTCTGTGGCT	180
Db	121	CCCGCTGCATCAAGGCCTACCCACTGTCTCCATGCTGGGCTCTCCCTGCCTTCTGTGGCT	180
Qy	181	CCTGGCCGTGACCTTCTTGGTTCCCGAGAGCTCAGCCCTTGGCCCCCTCAAGACTTTGAAGA	240
Db	181	CCTGGCCGTGACCTTCTTGGTTCCCGAGAGCTCAGCCCTTGGCCCCCTCAAGACTTTGAAGA	240
Qy	241	AGAGGAGGCAGATGAGACTGAGACGGCGTGGCCGCCTTTGCCGGCTGTCCCCTGCGACTA	300
Db	241	AGAGGAGGCAGATGAGACTGAGACGGCGTGGCCGCCTTTGCCGGCTGTCCCCTGCGACTA	300
Qy	301	CGACCACTGCCGACACCTGCAGGTGCCCTGCAAGGAGCTACAGAGGGTGGGGCCGGCGGC	360
Db	301	CGACCACTGCCGACACCTGCAGGTGCCCTGCAAGGAGCTACAGAGGGTGGGGCCGGCGGC	360
Qy	361	CTGCCTGTGCCCAGGACTCTCCAGCCCCGCCAGCCGCCGACCCGCCGCGCATGGGAGA	420
Db	361	CTGCCTGTGCCCAGGACTCTCCAGCCCCGCCAGCCGCCGACCCGCCGCGCATGGGAGA	420
Qy	421	AGTGCGCATTGCGGCCGAAGAGGGCCGCGCAGTGGTCCACTGGTGTGCCCCCTTCTCCCC	480
Db	421	AGTGCGCATTGCGGCCGAAGAGGGCCGCGCAGTGGTCCACTGGTGTGCCCCCTTCTCCCC	480
Qy	481	GGTCCTCCACTACTGGCTGCTGCTTTGGGACGGCAGCGAGGCTGCGCAGAAGGGGCCCCC	540
Db	481	GGTCCTCCACTACTGGCTGCTGCTTTGGGACGGCAGCGAGGCTGCGCAGAAGGGGCCCCC	540
Qy	541	GCTGAACGCTACGGTCCGAGAGCCGAAGTGAAGGGGCTGAAGCCAGGGGGCATTATATGT	600
Db	541	GCTGAACGCTACGGTCCGAGAGCCGAAGTGAAGGGGCTGAAGCCAGGGGGCATTATATGT	600
Qy	601	CGTTTTCGTAGTGGCCGCTAACGAGGCCGGGGCAAGCCGCGTGGCCAGGCTGGAGGAGA	660
Db	601	CGTTTTCGTAGTGGCCGCTAACGAGGCCGGGGCAAGCCGCGTGGCCAGGCTGGAGGAGA	660

